

From: Mertz, Prema
Sent: Tuesday, July 05, 2005 2:37 PM
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Thanks.

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Searcher: _____
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: July 9, 2005, 12:25:44 ; Search time 110.682 Seconds

(without alignments)
805.025 Million cell updates/sec

Title: US-10-751-242-1

Perfect score: 896
Sequence: 1 TELGPASSLPQSEFLKCLREQ.....SHLQSFLEVSRYVRLHLAGP 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	896	100.0	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.7	207	CSF3_HUMAN	P09919 homo sapien
3	744	83.0	194	CSF3_FELCA	O02708 felis silve
4	744	83.0	195	Q9GJ10	Q9GJ10 felis silve
5	738	82.4	174	CSF3_SHEEP	Q28746 ovis aries
6	734	81.9	175	CSF3_CANFA	P35834 canis fami
7	727	81.1	195	CSF3_BOVIN	P35833 bos taurus
8	702	78.3	195	CSF3_PIG	O02837 sus scrofa
9	641	71.5	208	CSF3_MOUSE	P09920 mus musculu
10	634	70.8	124	P97712	P97712 rattus norv
11	511	57.0	127	Q8MKE0	Q8MKE0 equus cabal
12	304	33.9	201	MGF_CHICK	P13854 gallus gall
13	111	12.3	241	Q90Y10	Q90Y10 gallus gall
14	110.5	12.3	212	Q8M775	Q8M775 sus scrofa
15	108	12.1	208	Q9X780	Q9X780 delphinape
16	106.5	11.9	212	IL6_PIG	P26893 sus scrofa
17	101	11.3	205	IL6_ORCOR	Q28747 orctinus orc
18	100	11.2	208	IL6_HORSE	Q95181 equus cabal
19	96	10.7	189	Q6N282	Q6N282 homo sapien
20	95	10.6	208	Q9H2A5	Q9H2A5 homo sapien
21	94.5	10.5	208	IL6_FELCA	P41683 felis silve
22	94.5	10.5	208	Q8D706	Q8D706 vibrato vuln
23	94	10.5	345	Q9KTL6	Q9KTL6 vibrato chol
24	93	10.4	189	Q9NPF7	Q9NPF7 homo sapien
25	91	10.2	214	Q6N280	Q6N280 homo sapien
26	89.5	10.0	214	Q8MKE5	Q8MKE5 sus scrofa
27	89.5	10.0	2175	HMCI_DROME	P10180 drosophila
28	88.5	9.9	666	Q9A523	Q9A523 caulobacter
29	88.5	9.9	786	Q91019	Q91019 pseudomonas
30	88.5	9.9	1931	Q8R0Y3	Q8R0Y3 stigmatalia
31	86	9.6	208	IL6_BOVIN	P26892 bos taurus

32	86	9.6	502	2	Q34008	Q34008 beta vulgar
33	86	9.6	788	2	Q8CF87	Q8CF87 mus musculu
34	86	9.6	850	2	Q7TQ21	Q7TQ21 mus musculu
35	86	9.6	851	2	Q8CF88	Q8CF88 mus musculu
36	86	9.6	852	2	Q811T9	Q811T9 mus musculu
37	85.5	9.5	211	2	Q865W7	Q865W7 camelus bac
38	85.5	9.5	1288	2	Q8LOR8	Q8LOR8 oryza sativ
39	85	9.5	193	2	Q9N2H9	Q9N2H9 sus scrofa
40	85	9.5	208	2	Q6V919	Q6V919 bubalus bub
41	84.5	9.4	209	1	IL6_PHOVI	Q28819 phoca vitul
42	84.5	9.4	211	1	IL6_LAMGL	Q865X6 lama glama
43	84.5	9.4	455	2	Q7MDW7	Q7MDW7 vibrato vuln
44	84	9.4	175	2	Q9TTH4	Q9TTH4 aotus nigri
45	84	9.4	208	1	IL6_CAPHI	Q28319 capra hircu

ALIGNMENTS

RESULT 1
Q8N4W3 PRELIMINARY; PRT; 200 AA.
AC Q8N4W3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Colony stimulating factor 3, isoform C.
GN Name=CSF3;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usetin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC03245; AAH3245.1; -
DR HSSP; P09919; IGNC.
DR GO; GO:0005576; C=extracellular; IEA.
DR GO; GO:0005125; F=cytokine activity; IEA.
DR GO; GO:0005138; F=interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P=immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF MGF.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN6.
 DR Prodom; PD008386; GCSF MGF: 1.
 DR Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE: 200 AA; 21543 MW; 8648AA5B329A96C CRC64;
 SO
 Query Match 100.0%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 5.2e-76;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPLGPASLPSQFLKCLEQVRKIQGDGAAIQKCATYKCHPELVLLGHSIGIPWAP 60
 DB 27 TPLGPASLPSQFLKCLEQVRKIQGDGAAIQKCATYKCHPELVLLGHSIGIPWAP 86
 QY 61 LSSCPQALQAGLSQHSGLFYQGLIQALGHSPELPLDVLQDVADPATTWQQ 120
 DB 87 LSSCPQALQAGLSQHSGLFYQGLIQALGHSPELPLDVLQDVADPATTWQQ 146
 QY 121 MEELGMAPALQPTQAMPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 174
 DB 147 MEELGMAPALQPTQAMPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 200
 RESULT 2
 CSF3_HUMAN STANDARD; PRT: 207 AA.
 AC P09919;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluriprotein)
 DE (Filgrastim) (Lenograstim).
 GN Name=CSF3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118679; PubMed=3484805;
 RA Nagata S., Teuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
 RT "Molecular cloning and expression of cDNA for human granulocyte
 RT colony-stimulating factor.";
 RL Nature 319:415-418 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86220137; PubMed=2423327;
 RA Nagata S., Teuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 RT colony-stimulating factor.";
 RL EMBO J. 5:575-581 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87196936; PubMed=3494801;
 RA Devlin J.J., Devlin P.E., Wyambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines.";
 RL J. Leukoc. Biol. 41:302-306 (1987).
 RN [4]
 RP SEQUENCE FROM N.A. AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carlington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "Seattlesp. NHBLI H6682 program for genomic applications, UW-
 RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE=86151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zeebo K.M.,

RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
 RA Barendt J., Platzer E., Moore M.A.S., Merzelmann R., Weite K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66 (1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293942; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62 (1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-W;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439 (1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304859; PubMed=7518249;
 RA Zink T., Ross A., Luers K., Gieslar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 RT bundle protein.";
 RL Biochemistry 33:8453-8463 (1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Oestlund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes/macrophages. This
 CC CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Even-Alternative splicing; Named isoforms=2;
 CC Name-long:
 CC IsoId=P09919-1; Sequence=displayed;
 CC Name-short:
 CC IsoId=P09919-2; Sequence=VSP_002673;
 CC -1- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -1- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -1- CAUTION: Ref.4 misquotes the gene name as "CSF1".
 CC -1- DATABASE: NMB=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="http://www.neupogen.com/".
 CC
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 CC -----
 CC EMBL; X03438; CAA27168.1; -
 CC EMBL; M13008; AAA03056.1; -
 CC EMBL; X03656; CAA27291.1; -
 CC EMBL; X03655; CAA27290.1; -

DR EMBL; AF388025; AAK62469.1; -
 DR EMBL; M17706; AAA5882.1; -
 DR PIR; A24573; A24573.
 DR PIR; A25093; FQHUOL.
 DR PDB; 1C09; X-ray; A/C=30-207.
 DR PDB; 1GNC; NMR; @=30-207.
 DR PDB; 1PGR; X-ray; A/C/E/G=30-207.
 DR PDB; 1RHG; X-ray; A/B/C=31-207.
 DR Genew; HGNC:2438; CSF3.
 DR MIM; 138970; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. .; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRODOM; PD008388; GCSF_MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR 3D-structure; Alternative splicing; Cytokine; Glycoprotein;
 KW Growth factor; Pharmaceutical; Polymorphism; Signal.
 FT CHAIN 1 30
 FT SIGNAL 1 30
 FT DISULFID 69 75
 FT DISULFID 97 107
 FT CARBOHYD 166 166
 FT VARSPPLIC 66 66
 FT VARIANT 157 157
 FT VARIANT 157 157
 FT VARIANT 174 174
 FT HELIX 41 65
 FT HELIX 69 71
 FT HELIX 77 86
 FT TURN 87 88
 FT HELIX 105 124
 FT TURN 125 127
 FT TURN 130 132
 FT HELIX 133 156
 FT TURN 157 158
 FT HELIX 176 203
 FT TURN 204 204
 SQ SEQUENCE 207 AA; 22293 MW; 421P635EC776996 CRC64;
 Query Match 98.7%; Score 884.5; DB 1; Length 207;
 Best Local Similarity 98.3%; Pred. No. 6.1e-73;
 Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 TPLGASSLPSPFLKLCLEQVRKIQGDGAALOEK---CATYKLCHEPELVLLGHSIGIP 57
 DB 31 TPLGASSLPSPFLKLCLEQVRKIQGDGAALOEKLVSECAITKLCHEPELVLLGHSIGIP 90
 QY 58 WAPLSSCSQALQAGLSQHSGLFLYQGLQALLEGISPELGPTLDTQLQDVADPATTI 117
 DB 91 WAPLSSCSQALQAGLSQHSGLFLYQGLQALLEGISPELGPTLDTQLQDVADPATTI 150
 QY 118 WQWHEELMAPALQTOGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAP 174
 DB 151 WQWHEELMAPALQTOGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAP 207
 RESULT 3
 CSF3_FELCA
 ID CSF3_FELCA STANDARD; PRT; 194 AA.
 AC 002708;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).

GN Name=CSF3;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=European shorthair; TISSUE=Lung;
 RX MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
 RA Dunham S.P.; Onions D.E.;
 RT "Isolation, nucleotide sequence and expression of a cDNA encoding
 RT feline granulocyte colony-stimulating factor";
 RL Cytokine 14:347-351(2001).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induces granulocytes (by similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; Y08558; CAA69853.1; -
 DR PIR; T09255; T09255.
 DR HSSP; P09919; IRHG.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR PRODOM; PD008388; GCSF_MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor; Signal.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT CHAIN 1 20
 FT SIGNAL 1 20
 FT DISULFID 21 194
 FT DISULFID 56 62
 FT CARBOHYD 84 94
 FT CARBOHYD 153 153
 SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DE7385E CRC64;
 Query Match 83.0%; Score 744; DB 1; Length 194;
 Best Local Similarity 81.0%; Pred. No. 4.2e-60;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 TPLGASSLPSPFLKLCLEQVRKIQGDGAALOEK---CATYKLCHEPELVLLGHSIGIP 60
 DB 21 TPLGFTSLPSPFLKLCLEQVRKIQGDGAALOEKCAHKKCHEPELVLLGHSIGIP 80
 QY 61 LSSCSQALQAGLSQHSGLFLYQGLQALLEGISPELGPTLDTQLQDVADPATTIWQ 120
 DB 81 LSSCSQALQAGLSQHSGLFLYQGLQALLEGISPELGPTLDTQLQDVADPATTIWQ 140
 QY 121 MEELGMAPALQTOGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAP 174
 DB 141 MEDVGMAPALQTOGAMPAPAFASAFORRAGGVIVASHLOSFLVSVYRVLRLHAP 194
 RESULT 4
 ID 09GJTO PRELIMINARY; PRT; 195 AA.
 AC 09GJTO
 DT 09GJTO

AC 09GJ0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DB Granulocyte colony-stimulating factor precursor.
 GN Name=G-CSF;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21531548; PubMed=11675019; DOI=10.1016/S0378-1119(01)00575-3;
 RA Yamamoto A., Iwata A., Tsuchiya K., Katsumata A., Oishi K., Saito T.,
 RA Tsujimoto H., Hasegawa A., Ueda S.;
 RT "Molecular cloning and expression of the cDNA encoding feline
 RT granulocyte colony-stimulating factor.";
 RT Gene 274:263-269(2001).
 RL EMBL; AB042552; BAB17789.1;
 DR EMBL; AB042552; BAB17789.1;
 DR HSSP; P35834; 1BGF.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 195 AA; 21255 MW; 5440682909412FCF CRC64;
 Query Match 83.0%; Score 744; DB 2; Length 195;
 Best Local Similarity 81.0%; Pred. No. 4.2e-60;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 QY 1 TPGLPSSLPSPFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVILGSHGIPAP 60
 DB 22 TPLGTSLSLPSPFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVILGSHGIPAP 81
 QY 61 LSSCPQALQAGCLSQLHSGFLFYQGLQLQALEGISPELGPTLDTLQDVADPATTIWQ 120
 DB 82 LSSCSQALQAGCLSQLHSGFLFYQGLQLQALEGISPELGPTLDTLQDVADPATTIWQ 141
 QY 121 MEELGMAPALOPTGAMPAPASAFORRAGGTVLVASHLSFLEVSRYVRLHQAOP 174
 DB 142 MEDVGMAPAVPPTGTMPTFTSAFORRAGGTVLVASHLSFLEVSRYVRLHQAOP 195

RESULT 5

CSF3_SHEEP
 ID CSF3_SHEEP STANDARD; PRT; 174 AA.
 AC Q28746;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Granulocyte colony-stimulating factor (G-CSF).
 GN Name=CSF3;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95102116; PubMed=7528579;

RA O'Brien P.M., Seow H.F., Rothel J.S., Wood P.R.;
 RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
 RT factor cDNA."
 RL DNA Seq. 4:339-342(1994).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induces granulocytes (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; L07939; AAA68006.1;
 DR EMBL; L07939; AAA68006.1;
 DR PIR; T10268; T10268.
 DR HSSP; P09919; 1RHG.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor.
 KM DLSLFTD 36 42 By similarity.
 FT DISULFTD 64 74 By similarity.
 FT CARBOHYD 133 133 O-linked (GalNAc... (By similarity).
 SQ SEQUENCE 174 AA; 18806 MW; BAA5A8F8D23ACDIE CRC64;
 Query Match 82.4%; Score 738; DB 1; Length 174;
 Best Local Similarity 82.2%; Pred. No. 1.3e-59;
 Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
 QY 1 TPGLPSSLPSPFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVILGSHGIPAP 60
 DB 1 TPLGTSLSLPSPFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVILGSHGIPAP 60
 QY 61 LSSCPQALQAGCLSQLHSGFLFYQGLQLQALEGISPELGPTLDTLQDVADPATTIWQ 120
 DB 61 LSSCSQALQAGCLSQLHSGFLFYQGLQLQALEGISPELGPTLDTLQDVADPATTIWQ 120
 QY 121 MEELGMAPALOPTGAMPAPASAFORRAGGTVLVASHLSFLEVSRYVRLHQAOP 174
 DB 121 MEDVGMAPAVPPTGTMPTFTSAFORRAGGTVLVASHLSFLEVSRYVRLHQAOP 174

RESULT 6

CSF3_CANFA
 ID CSF3_CANFA STANDARD; PRT; 175 AA.
 AC P35834;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DB Granulocyte colony-stimulating factor (G-CSF).
 GN Name=CSF3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=94076341; PubMed=7504736;
 RX Lovejoy B., Cascio D., Eisenberg D.;

RT		"Crystal structure of canine and bovine granulocyte-colony-stimulating factor (G-CSF).";
RJ	J. Mol. Biol.	234:640-653(1993).
CC	-I-	FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
CC	-I-	SUBUNIT: Monomer.
CC	-I-	SUBCELLULAR LOCATION: Secreted.
CC	-I-	PTM: O-glycosylated.
CC	-I-	SIMILARITY: Belongs to the IL-6 superfamily.
DR	PDB:	1BGD; X-ray; @=1-175.
DR	PDB:	1BGE; X-ray; A/B=1-175.
DR	InterPro:	IPR009079; 4_helix_cytokine.
DR	InterPro:	IPR003629; GCSF_MGF.
DR	InterPro:	IPR003573; IL6_MGF_GCSF.
DR	Pfam:	PF00489; IL6_1.
DR	PRINTS:	PR00433; IL6GCSFMGF.
DR	ProDom:	PD008388; GCSF_MGF; 1.
DR	SMART:	SM00126; IL6; 1.
DR	PROSITE:	PS00254; INTERLEUKIN_6; 1.
KW	3D-structure;	Cytokine; Glycoprotein; Growth factor.
FT	DISULFID	37 43
FT	DISULFID	65 75
FT	CARBOHYD	134 134
FT	STRAND	10 10
FT	HELIX	12 39
FT	HELIX	45 55
FT	TURN	56 56
FT	HELIKX	63 65
FT	TURN	67 69
FT	HELIX	72 92
FT	TURN	93 95
FT	TURN	98 100
FT	HELIX	101 125
FT	TURN	126 126
FT	HELIKX	144 171
FT	TURN	172 172
FT	STRAND	173 173
SQ	SEQUENCE	175 AA; 18858 MW; 28C36B24990C6DB3 CRC64;
Query Match 81.9%; Score 734; DB 1; Length 175;		
Best Local Similarity 80.9%; Pred. No. 3.1e-59;		
Matches 140; Conservative 11; Mismatches 22; Indels 0; Gaps 0.		
OY	2	PLGPASLSPOSFLNCLCEOVRIKIQGDGAIOEKATCATVLCCHPEELVLIGHSIGPMPL 61
DB	3	PLGPGPGLPQSLLKLCKLEQMRVVDGTLQETLCAHOLCHPEELVVLGHNLGIPIPL 62
OY	62	SSCPESQALQLAGCLSQLSHSGFLFYOGILLQALAGISPELGPTLDLTQLDVADPATTIWOM 121
DB	63	SSCSSQALQLMGCLAQHSHSGFLFYOGILLQALAGISPDLAFTLDITQLDTTPPAIIWOM 122
OY	122	EELGNAPALOPTGAMPAPAFASFORRAGGVIVASHIQSFLEVSYRVLRHLAQP 174
DB	123	EDLGNAPAVPPTGTMPAFTSAFORRAGGVIVASNISFLRLAYRALRRFAKP 175
RESULT 7		
CSF3_BOVIN	STANDARD;	PRT; 195 AA.
ID	CSF3_BOVIN	
AC	P35833; Q9TV89;	
DT	01-JUN-1994 (Rel. 29, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DE	Granulocyte colony-stimulating factor precursor (G-CSF).	
DN	Name=CSF3; Synonyms=GCSF;	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovinae; Bos.	
NCBI_Taxid=9913;		

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RP RN [1] SEQUENCE FROM N.A.
RC RC STRAIN-Holstein;
RA RA Heidar M., Kehri M.E. Jr.;
RT RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RT RT colony stimulating factor.";
RL RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
RN RN [2]
RX RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RA RA MEDLINE=94076341; PubMed=7504736;
RT RT Lovejoy B., Cascio D., Eisenberg D.;
RT RT "Crystal structure of canine and bovine granulocyte-colony stimulating
RT RT factor (G-CSF).";
RL RL J. Mol. Biol. 234:640-653(1993).
CC CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC CC cytokines that act in hematopoiesis by controlling the production,
CC CC differentiation, and function of 2 related white cell populations
CC CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CC CSF induces granulocytes.
CC CC -1- SUBUNIT: Monomer.
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- PTM: O-glycosylated.
CC CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC CC -----
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CC CC -----
DR DR EMBL; AF092533; AAD16102.1; -.
DR DR PDB; 1BGC; X-ray; @=22-195.
DR DR InterPro; IPR003079; 4_helix_cytokine.
DR DR InterPro; IPR003629; GCSF_MGF.
DR DR InterPro; IPR003573; IL6_MGF_GCSF.
DR DR Pfam; PF00489; IL6; 1.
DR DR PRINTS; PR00433; IL6GCSFMGF.
DR DR PRODOM; PD008388; GCSF_MGF; 1.
DR DR SMART; SM00126; IL6; 1.
DR DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW KW 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT FT SIGNAL 1 21 Potential.
FT FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT FT DISULFID 57 63.
FT FT DISULFID 85 95
FT FT CARBOHYD 154 154 O-linked (GalNAc... ) (By similarity).
FT FT CONFLICT 93 94 TS -> RG (in Ref. 2).
FT FT HELIX 32 60
FT FT HELIX 65 69
FT FT TURN 70 71
FT FT HELIX 72 75
FT FT HELIX 76 76
FT FT TURN 83 85
FT FT HELIX 87 89
FT FT TURN 92 112
FT FT HELIX 113 115
FT FT TURN 118 120
FT FT HELIX 121 145
FT FT HELIX 164 191
FT FT HELIX 192 192
SQ SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFB73 CRC64;

Query March 81.1%; Score 727; DB 1; Length 195;
Best Local Similarity 81.0%; Pred. No. 1.5e-58;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Cy 1 TPILGPSASSLPQSTFLKCLEQVRIKIQSDGALQKRLCATYRLCHPEELVILGHSIGLIPWAP 60
Db 22 TPIGPSASSLPQSTFLKCLEQVRIKIQSDGALQKRLCAHRLCHPEELMLRRHSIGLIPQAP 81
Dy 61 LSSCPQALQALQACLSQHLGFLVYQGLIQALEGISPELQPTIDTQLQDVADFAITTIWQ 120

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Db 82 LSSSSSLQSTLQNLHGLFLYQGLQALAGISPELALDTLQADVDPATNTIMLQ 141
Qy 121 MEELGMAPALOPTGAMPAPASAFORRAGGVLVASHLOSFEVSVRYLRHIAOP 174
Db 142 MEDGAPAPVPTQGTAMPFTSAFORRAGGVLVASHLOSFEVSVRYLRHIAEP 195

RESULT 8
CSF3_PIG STANDARD; PRT; 195 AA.
ID CSF3_PIG STANDARD; PRT; 195 AA.
AC 002837; 019180; (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN 11
RP SEQUENCE FROM N.A.
RA Kilmburg P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gloster S.E.; Sandeman R.M.; Strom A.D.G.;
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
stimulating factor";
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL; Y10494; CAA71518.1; -
DR EMBL; U68482; AAB70701.1; -
DR EMBL; U68481; AAB70700.1; -
DR HSSP; P09919; IRHG.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6_1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 1 21 Potential.
FT DISULFID 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63 By similarity.
FT CARBOHYD 85 95 By similarity.
FT CONFLICT 123 123 O-linked (GalNAc... ) (By similarity).
SQ SEQUENCE 195 AA; 21214 MW; 84787F20DB0A8A1C CAC64;
Query Match 78.3%; Score 702; DB 1; Length 195;
Best Local Similarity 79.2%; Pred. No. 3e-56;

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Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
Qy 2 PLGPASSLPSFLKLCLEQVRKTIQGDGALOEKICATYKICHPBELVTLGHSIGIPWAPL 61
Db 23 PLSPASSLPSPFLKLCLEQVRKTIQADBAEIOERLCATKICHOELVTLGHSIGLPQASL 82
Qy 62 SSCPSQALQAGCLSQSHGLFLYQGLQALAGISPELALDTLQADVDPATNTIMQ 121
Db 83 SSCSSQALQTLGCLNQHGLVLYQGLQALAGISPELALDTLQADVDPATNTIMQ 142
Qy 122 MEELGMAPALOPTGAMPAPASAFORRAGGVLVASHLOSFEVSVRYLRHIAOP 174
Db 143 EDLMAPASLPPTQGTVPFTSAFORRAGGVLVASHLOSFEVSVRYLRHIAEP 195

RESULT 9
CSF3_MOUSE STANDARD; PRT; 208 AA.
ID CSF3_MOUSE STANDARD; PRT; 208 AA.
AC P09920;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=Csf3; Synonyms=Csf3;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=87017003; Pubmed=3489940;
RX Tauchiya M., Asano S., Kaziro Y., Nagata S.;
RT "Isolation and characterization of the cDNA for murine granulocyte
colony-stimulating factor";
RT Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87190474; Pubmed=3494605;
RA Tauchiya M., Kaziro Y., Nagata S.;
RT "The chromosomal gene structure for murine granulocyte colony-
stimulating factor";
RT Eur. J. Biochem. 165:7-12(1987).
[3]
RP PARTIAL SEQUENCE.
RX Pubmed=3501294;
RA Simpson R.J., Nice E.C., Nicola N.A.;
RT "Structural studies on the murine granulocyte colony-stimulating
factor";
RT Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL; M13926; AAA37672.1; -
DR EMBL; X05402; CAA28986.1; -
DR PIR; A29536; A26496.
DR HSSP; P09919; IRHG.
DR InterPro; IPR009079; 4_helix_cytokine.

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DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD008388; GCSF_MGF; 1.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR Cytokine: Direct protein sequencing; Glycoprotein; Growth factor;
KW Signal.
FT CHAIN 1 30 Granulocyte colony-stimulating factor.
FT DISUFID 72 By similarity.
FT DISUFID 100 By similarity.
FT CARBOHYD 169 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 208 AA; 22421 MW; 0BF3622135C906DB CRC64;

Query Match 71.5%; Score 641; DB 1; Length 208;
Best Local Similarity 75.9%; Pred. No. 1.2e-50;
Matches 129; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

QY 3 LGPASSLPQSFLLKCLEQVARKIQDGAALQEKLCATYKLCHEPELVLLGSLGIPWAPLS 62
DB 39 LPPSLPLPRSFLLKSLQVARKIQASGVLEQLCATYKLCHEPELVLLGSLGIPKASLS 98
QY 63 SCPSQALQAGCISQLSHSGFLFYQGLIQALEGISPELPTLDLTQLDVADPATTIWOOME 122
DB 99 GCSQALQOQTCISQLSHSGFLFYQGLIQALSGISPALAPTLTLDLVANPATTIWOOME 158

QY 123 ELGMAPALOPTOGAMPAPAFASAFORRAGGVVASHLOSFLVSRVLRHLA 172
DB 159 SLGVAFLVQPTQSTMPFTSAFRRAGGVVLTYSILOFLETAHALHLLRP 208

RESULT 10
P97712 PRELIMINARY; PRT; 214 AA.
ID P97712
AC P97712;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte colony stimulating factor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074556; PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
RA Han S.W., Ramash N., Osborne W.R.;
RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
stimulating factor."
RL Gene 175:101-104(1996).
DR EMBL: U37101; AAC52915.1; -.
DR PIR: JCS043; JCS043.
DR HSSP: P09919; IRRG.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD008388; GCSF_MGF; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match 70.8%; Score 634; DB 2; Length 214;
Best Local Similarity 73.8%; Pred. No. 5.6e-50;
Matches 127; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

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QY 3 LGPASSLPQSFLLKCLEQVARKIQDGAALQEKLCATYKLCHEPELVLLGSLGIPWAPLS 62
DB 30 LPPSLPLPRSFLLKSLQVARKIQARTELEQLCATYKLCHEPELVLLGSLGIPKASLS 89
QY 63 SCPSQALQAGCISQLSHSGFLFYQGLIQALEGISPELPTLDLTQLDVADPATTIWOOME 122
DB 90 SCSSQALQOQTCISQLSHSGFLFYQGLIQALSGISSELPATLMDLMDLVANPATTIWOOME 149

QY 123 ELGMAPALOPTOGAMPAPAFASAFORRAGGVVASHLOSFLVSRVLRHLAOP 174
DB 150 SLGVAFLVQPTQSTMPFTSAFRRAGGVVLTYSILOFLETAHALHLLRP 201

RESULT 11
QMKRO
ID QMKRO PRELIMINARY; PRT; 127 AA.
AC QMKRO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte colony-stimulating factor.
GN Name=G-CSF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Noronha L.B., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF503365; AAM34205.1; -.
DR HSSP: P35833; IBCG.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD008388; GCSF_MGF; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match 57.0%; Score 511; DB 2; Length 127;
Best Local Similarity 79.5%; Pred. No. 5.9e-39;
Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 48 VLLGSHSGIPWAPLSQSSQALQAGCISQLSHSGFLFYQGLIQALEGISPELPTLDLTQ 107
DB 1 KLLGSHSGIPWAPLSQSSQALQAGCISQLSHSGFLFYQGLIQALSGISSELPATLMDMQ 60
QY 108 LDVADPATTIWOOMEELGMAPALOPTOGAMPAPAFASAFORRAGGVVASHLOSFLVSRV 167
DB 61 LDVTPATTIWOOMEDLGVAFLVQPTQSTMPFTSAFRRAGGVVASHLOSFLVSRV 120
QY 168 LRLHAOP 174
DB 121 LRYLAEP 127

RESULT 12
MGF_CHICK
ID MGF_CHICK STANDARD; PRT; 201 AA.
AC P13854;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myelomonocytic growth factor precursor (MGF).
OS Gallus gallus (Chicken).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89231616; PubMed=2785450;
 RA Leutz A., Damm K., Sternack E., Kowenz E., Nees S., Frank R.,
 RA Gauspohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.,
 RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
 RT reveals relationship to interleukin 6 and granulocyte colony
 RT stimulating factor";
 RL EMBO J. 8:175-181(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92195319; PubMed=1549124;
 RA Sternack E., Blattner C., Graf T., Leutz A.,
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases";
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -1- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 DR EMBL: M85034; AAA8694.1; -;
 DR EMBL: X14477; CA32639.1; -;
 DR PIR: A42247; A42247.
 DR HSSP: P09919; IHMG.
 DR InterPro: IPR009079; 4 helix cytokine.
 DR InterPro: IPR003629; GCSF_MGF.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD008388; GCSF_MGF; 1.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR SMART: PS00254; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Glycoprotein; Growth factor; Signal.
 FT CHAIN 1 23
 FT DISULFID 24 201 Myelomonocytic growth factor.
 FT DISULFID 61 67 By similarity.
 FT CARBOHYD 89 99 By similarity.
 FT CARBOHYD 123 123 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 201 AA; 22373 MW; 240A8DD21B424486 CRC64;
 Query Match 33.9%; Score 304; DB 1; Length 201;
 Best Local Similarity 40.6%; Pred. No. 9; 1e-20;
 Matches 67; Conservative 28; Mismatches 68; Indels 2; Gaps 1;
 QY 11 QSFLLKLEQVRKIQGDGAALQKLCATYKLCHEBELVLLGSLGIPWAPLSSCPQALQ 70
 DB 36 QLFHLKLEFRKIRGDUVAALQRAVCDTFLCTEELQLVOPDPLVQAPDQGHKGFQ 95
 QY 71 LAGCLSGHSGLPFYQGLQALBESIPBLPTDLOLVADFAFTTITWQMBELGMAPAL 130
 DB 96 AEVCFQIRAGLAHVDSLGAVRLPLPHHTTVLTLQDDAANSSNQOQMEDGLDVT 155
 QY 131 QPTQ--GAPPAFAFORBAGVVLASHLQSFLEVSRYRLHLAQ 173

DB 156 LPAEQSPPTFSGPFQOQVGFPIIANFORFLETAYRALRHILAR 200
 RESULT 13
 ID 090Y10 PRELIMINARY; PRT; 241 AA.
 AC 090Y10;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Name-IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.,
 RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.,
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by *Salmonella typhimurium*, *Salmonella enteritidis* and
 RT *Salmonella gallinarum*";
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kaiser P.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ209540; CAC40812.1; -;
 DR EMBL: AJ20838; CAC15566.2; -;
 DR HSSP: P05231; IALU.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD008388; GCSF_MGF; 1.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR SMART: PS00254; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Signal.
 FT CHAIN 1 47 Potential.
 FT CHAIN 48 241 mature ChIL-6.
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 Query Match 12.4%; Score 111; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.053;
 Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;
 QY 3 LGPASPSP-----QSFLLKLEQVRKIQGDGAALQKLCATYKLC 43
 DB 41 LPPAAVPLPAAADSGEVLGEERAGARRLLDCEPLARYLRRAVQLODECKKFTVCE 100
 QY 44 PEELVLLGSLGIPWAPLSSCPQALQALG-----CLSGHSGLPFYQGLQALBESIP 98
 DB 101 NSMEVLVRNNLNP-----KTEEDGCLLAGFDEKCLTKLSGLPFAQTYLRFIQTFDS 156
 QY 99 LGPTLDTLOLVADFAFTTITWQMBELGMAPALOPTQGAAPAFASAFORBAGVVL----- 152
 DB 157 EKQNVESLQYSGHLAATIRQNV-----INPDEVLP--DQAQKSLANIKSDXW 206
 QY 153 ---VASHL-----QSFLEVSRYRLHL 171
 DB 207 IEKTIWHLIIRDTSPMEKTVRAVRYL 233

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RESULT 14
Q8MJ75 PRELIMINARY; PRT; 212 AA.
ID Q8MJ75
AC Q8MJ75;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AF518322; AM74938.1; -.
DR HSSP: P05231; 1ALU.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:Cytokine activity; IEA.
DR GO: GO:0005138; F:Interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:Immune response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR003573; IL6 MGF GCSE.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRODOM: PD004356; INTERLEUKIN_6.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E703BCFD77 CRC64;

Query Match 12.3%; Score 110.5; DB 2; Length 212;
Best Local Similarity 23.3%; Pred. No. 0.052;
Matches 37; Conservative 32; Mismatches 85; Indels 5; Gaps 3;

QY 16 KCLGVKTIQGDGALQKLCATYKLCHEPELVILGHSIGIP-WAPLSSCPGQALQAGLSQ 74
DB 52 KTEELIKYILGKISAMREMECEKYCKENSKENSVLAENNLNPKMAEKDGCFOGSGFNOETC 111
QY 75 LSGHSGFLVYQGLQALBEGISPELGPTLDLTQLDVADPATTIWOQMEELGAPALOPT- 133
DB 112 LKRTITGVLFQYLDYLVQNEYESNKGAVQISTKALIQTLRQKGNPKATTPPTT 171
QY 134 -OGAMPAPAS--AFORRAGGVLVASHLOSFLVSYRVLR 169
DB 172 NAGLDDKQSQNEMMNTKIILIRSLDFLQFSLRAIR 210

RESULT 15
Q9XT80 PRELIMINARY; PRT; 208 AA.
ID Q9XT80
AC Q9XT80;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., Archambault D.;
RL "Molecular cloning, phylogenetic analysis and expression of beluga
whale (Delphinapterus leucas) interleukin 6."
EMBL: AF076643; AAD42929.1; -.
DR HSSP: P05231; 1ALU.
DR GO: GO:0005576; C:extracellular; IEA.

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DR GO: GO:0005125; F:Cytokine activity; IEA.
DR GO: GO:0005138; F:Interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:Immune response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR003573; IL6 MGF GCSE.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRODOM: PD004356; INTERLEUKIN_6.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85CE80389C4 CRC64;

Query Match 12.3%; Score 108; DB 2; Length 208;
Best Local Similarity 21.3%; Pred. No. 0.086;
Matches 33; Conservative 35; Mismatches 81; Indels 6; Gaps 2;

QY 21 VKRIQGDGALQKLCATYKLCHEPELVILGHSIGIP-WAPLSSCPGQALQAGLSQ 79
DB 52 IKYILGKISAMREMECEKYCKENSKENSVLAENNLNPKMAEKDGCFOGSGFNOETC 111
QY 80 SGLFLVYQGLQALBEGISPELGPTLDLTQLDVADPATTIWOQMEELGAPALOPTQGA--- 136
DB 112 TGLLEIYQYLDYLVQNEYESNKGAVQISTKALIQTLRQKGNPKATTPPTT 171
QY 137 --MPAPASAFORRAGGVLVASHLOSFLVSYRVLR 169
DB 172 NNLQSQNDMMRNTKIILIRSLDFLQFSLRAIR 206

```

Search completed: July 9, 2005, 12:39:02
 Job time : 110.682 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 12:25:44 ; Search time 111.318 Seconds
(without alignments)
805.025 Million cell updates/sec

Title: US-10-751-242-2

Perfect score: 901
Sequence: 1 MTPGLPASSLPSQFLKCLE.....SHLQSFLEYSYRVLRHIAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	896	99.4	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.2	207	CSF3_HUMAN	P09919 homo sapien
3	744	82.6	194	CSF3_FELCA	002708 felis silve
4	744	82.6	195	Q9GJ10	09GJ10 gallus gall
5	739	82.0	175	CSF3_CANFA	P35834 canis famill
6	738	81.9	174	CSF3_SHEEP	Q28746 ovis aries
7	727	80.7	195	CSF3_BOVIN	P35833 bos taurus
8	702	77.9	195	CSF3_BOVIN	002837 sus scrofa
9	642	71.3	208	CSF3_MOUSE	P09920 mus muscula
10	635	70.5	214	P97712	P97712 rattus norv
11	511	56.7	127	Q8MKE0	Q8MKE0 equus cabal
12	504	33.7	201	MGF_CHICK	P13554 gallus gall
13	111	12.3	241	Q90Y10	Q90Y10 gallus gall
14	110.5	12.3	212	Q8M475	Q8M475 sus scrofa
15	108	12.0	208	Q9X780	Q9X780 delphinape
16	106.5	11.8	212	IL6_PIG	P26893 sus scrofa
17	101	11.2	205	IL6_ORCOR	Q28747 orctinus orc
18	100	11.1	208	IL6_HORSE	Q95181 equus cabal
19	96	10.7	189	Q6N282	Q6N282 homo sapien
20	96	10.7	189	Q6N282	Q6N282 homo sapien
21	95	10.5	208	IL6_FELCA	Q9180 felis silve
22	94.5	10.4	345	Q8D706	Q8D706 vibrio vuln
23	94	10.4	345	Q9K116	Q9K116 vibrio chol
24	93	10.3	189	Q9NPF7	Q9NPF7 homo sapien
25	91	10.1	189	Q6N280	Q6N280 homo sapien
26	89.5	9.9	214	Q8MKE5	Q8MKE5 sus scrofa
27	89.5	9.9	2175	HMCC DROME	P10180 drosophila
28	88.5	9.8	666	Q9A523	Q9A523 caulobacter
29	88.5	9.8	786	Q91019	Q91019 pseudomonas
30	88.5	9.8	1931	Q8K0Y3	Q8K0Y3 stigmatalia
31	88	9.8	290	Q9P0S7	Q9P0S7 homo sapien

32	86	9.5	208	116_BOVIN	P26892 bos taurus
33	86	9.5	502	Q34008	Q34008 beta vulgar
34	86	9.5	788	Q8CP87	Q8CP87 mus musculu
35	86	9.5	850	Q7TQ21	Q7TQ21 mus musculu
36	86	9.5	851	Q8CP88	Q8CP88 mus musculu
37	86	9.5	852	Q811T9	Q811T9 mus musculu
38	85.5	9.5	211	Q865W7	Q865W7 camelus bac
39	85.5	9.5	1288	Q8LQ88	Q8LQ88 oryza sativ
40	85	9.4	193	Q9N2H9	Q9N2H9 sus scrofa
41	85	9.4	208	Q6V919	Q6V919 bubalus bub
42	84.5	9.4	209	116_PROVI	Q28819 phoca vitul
43	84.5	9.4	211	IL6_TAMGL	Q865K6 lama glama
44	84.5	9.4	455	Q7MDW7	Q7MDW7 vibrio vuln
45	84	9.3	175	Q9TTH4	Q9TTH4 actus nigri

ALIGNMENTS

RESULT 1	ID	Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC	Q8N4W3				
DT	01-OCT-2002 (TREMblrel. 22, Created)				
DT	01-OCT-2002 (TREMblrel. 22, Last sequence update)				
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)				
DE	Colony stimulating factor 3, isoform C.				
GN	Name=CSF3;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid:9606;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RA	Strausberg R.,				
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC033245; AAH3245.1; -				
DR	HSSP; P09919; IGNC.				
DR	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0005125; F:cytokine activity; IEA.				
DR	GO; GO:0005138; F:interleukin-6 receptor binding; IEA.				
DR	GO; GO:0006955; P:immune response; IEA.				
DR	InterPro; IPR009079; I:4 helix cytokine.				
DR	InterPro; IPR003629; GCSF_MGF.				
DR	InterPro; IPR003573; IL6_MGF_GCSF.				
DR	InterPro; IPR003574; Interleukin_6.				
DR	Pfam; PF00489; IL6; 1.				
DR	PRINTS; PR00433; IL6GCSFMGF.				

PRINTS: PR00434, INTERLEUKIN6.
 DR PRODOM; PD006388; GCSF MGF: 1.
 DR PRODOM; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN 6; 1.
 DR SEQUENCE 200 AA; 21543 MW; 8648A55B329A96C CRC64;
 Query Match 99.4%; Score 896; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6.9e-74;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TPLGPSASLPQSFLLKLEQVRKIQGDALQOEKLCATYKLCHEPELVLLGHSIGIPWAP 61
 DB 27 TPLGPSASLPQSFLLKLEQVRKIQGDALQOEKLCATYKLCHEPELVLLGHSIGIPWAP 86
 QY 62 LSSCPGQALQAGCLSQLHSGFLYQGLQALBESISELPPTDLOLDVADPATTTWQ 121
 DB 87 LSSCPGQALQAGCLSQLHSGFLYQGLQALBESISELPPTDLOLDVADPATTTWQ 146
 QY 122 MEELGAPALQPTQGMARFAPAFORAGGVVAASHQSLFVSYRLRLAQP 175
 DB 147 MEELGAPALQPTQGMARFAPAFORAGGVVAASHQSLFVSYRLRLAQP 200
 RESULT 2
 CSF3_HUMAN STANDARD; PRT; 207 AA.
 ID CSF3_HUMAN P09919;
 AC P09919;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripolietin)
 DE (Flgrastim) (lenograstim).
 GN Name=CSF3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118679; PubMed=3484805;
 RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
 RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
 RT "Molecular cloning and expression of cDNA for human granulocyte
 RT colony-stimulating factor.";
 RL Nature 319:415-418(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86220137; PubMed=2423327;
 RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T., Yamamoto O., Hirata Y., Kubota N.,
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 RT colony-stimulating factor.";
 RL EMBO J. 5:575-581(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87196936; PubMed=3494801;
 RA Devlin J.J., Devlin P.E., Wyambo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 RT lines.";
 RL J. Leukoc. Biol. 41:302-306(1987).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattlesNP5. NHLBI HU6682 program for genomic applications, UW-
 RT FHCRG, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE=86151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zeebo K.M.,

Murdoch D.C., Chazin V.R., Brzezewski J., Lu H., Chen K.K.,
 RA Barendt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66(1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293942; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62(1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439(1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304859; PubMed=7518249;
 RA Zink T., Ross A., Inerts K., Cieslar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 RT bundle protein.";
 RL Biochemistry 33:8453-8463(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Osblund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 CC cytokines that act in hematopoiesis by controlling the production,
 CC differentiation, and function of 2 related white cell populations
 CC of the blood, the granulocytes and the monocytes-macrophages. This
 CC CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=P09919-1; Sequence=Displayed;
 CC Name=short;
 CC IsoId=P09919-2; Sequence=VSP_002673;
 CC -1- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
 CC modified with up to two sialic acid residues (done in
 CC recombinantly expressed G-CSF from CHO cells).
 CC -1- PHARMACOLOGICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Kochne) and Granocyte (Rhône-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -1- CAUTION: Ref 4 misquotes the gene name as "CSF1".
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="http://www.neupogen.com/".
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 CC or send an email to license@sib-sib.ch).
 DR EMBL: X03438; CAA27168.1; -
 DR EMBL: M13008; AAA03056.1; -
 DR EMBL: X03656; CAA27291.1; -
 DR EMBL: X03655; CAA27290.1; -

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AC 09GUU0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN Name=G-CSF;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21531548; PubMed=11675019; DOI=10.1016/S0378-1119(01)00575-3;
RA Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Gene 274:263-269(2001).
DR EMBL; AB042552; BAB17789.1; -.
DR EMBL; AB042553; BAB17757.1; -.
DR HSSP; P35834; 1BGE.
DR GO; GO:0005576; C:cytoregulatory; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0005138; P:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SIGNAL.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412FCF CRC64;

Query Match 82.6%; Score 744; DB 2; Length 195;
Best Local Similarity 81.0%; Pred. No. 5,4e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPLGASSLPQSFLKLCIEQVRKIQGDGAALOELCATYKLCHEBELVILGSHGIPWA 61
DB 22 TPLGSSLPQSFLKLCIEQVRKVQADGTALQETLCANHLCHPEBELVILGHALGIPQAP 81
QY 62 LSSCPSQALQAGCLSQLHSGFLFYQGLQALEGISPELGPTDPTQLDVADPATITWQ 121
DB 82 LSSCPSQALQAGCLSQLHSGFLFYQGLQALAGISPELAPTLDMQLDITDPAINIWQ 141
QY 122 MEELGMAPALOPTOGAMPAPASAFORRAGGVLVASHQSFLEVSRYVLRHLAOP 175
DB 122 MEDVGMAPAVPPTGTGMPPTTSAFORRAGGTLVASHQSFLEVAAYALRHFTKP 195

RESULT 5
CSF3_CANFA STANDARD; PRT; 175 AA.
ID CSF3_CANFA
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;

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RT "Crystal structure of canine and bovine granulocyte-colony stimulating
RT factor (G-CSF).";
RL J. Mol. Biol. 234:640-653(1993).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
DR PDB; 1BGD; X-ray; @=1-175.
DR PDB; 1BGE; X-ray; A/B=1-175.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KM 3D-structure; Cytokine; Glycoprotein; Growth factor.
FT DISULFID 37 43
FT DISULFID 65 75
FT CARBOHYD 134 134 O-linked (GalNAc...) (By similarity).
FT STRAND 10 10
FT HELIX 12 39
FT HELIX 45 55
FT TURN 56 56
FT HELIX 63 65
FT TURN 67 69
FT HELIX 72 92
FT TURN 93 95
FT TURN 98 100
FT TURN 101 125
FT TURN 126 126
FT TURN 144 171
FT HELIX 172 172
FT STRAND 173 173
SQ SEQUENCE 175 AA; 18858 MW; 28C26B24990C6DB3 CRC64;

Query Match 82.0%; Score 739; DB 1; Length 175;
Best Local Similarity 80.6%; Pred. No. 1,4e-59;
Matches 141; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

QY 1 MTPLGASLPQSFLKLCIEQVRKIQGDGAALOELCATYKLCHEBELVILGSHGIPWA 60
DB 1 MAPLGPTGLPQSFLKLCIEQVRKVQADGTALQETLCATQLCHEBELVILGHALGIPQ 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLQALEGISPELGPTDPTQLDVADPATITWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLQALAGISPELAPTLDMQLDITDPAINIWQ 120
QY 121 MEELGMAPALOPTOGAMPAPASAFORRAGGVLVASHQSFLEVSRYVLRHLAOP 175
DB 121 QMEDLGMAPAVPPTGTGMPPTTSAFORRAGGTLVASHQSFLEVAAYALRHFTKP 175

RESULT 6
CSF3_SHEEP STANDARD; PRT; 174 AA.
ID CSF3_SHEEP
AC Q28746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprine; Ovis.
OX NCBI_TaxID=9940;

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RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95102116; PubMed=7528579;
 RA O'Brien P.M., Seow H.F., Roedel J.S., Wood P.R.;
 RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
 factor cDNA."
 RL DNA Seq. 4:339-342(1994).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: I07939; AAA68006.1; -
 CC PIR: T10268; T10268.
 CC HSSP: P09919; 1RHG.
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003629; GCSF_MGF.
 CC InterPro: IPR003573; IL6_MGF_GCSF.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC ProDom: PD008388; GCSF_MGF; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Cytokine; Glycoprotein; Growth factor.
 CC DISULFID 36 42 By similarity.
 CC FT DISULFID 64 74 By similarity.
 CC CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
 CC SEQUENCE 174 AA; 18806 MW; BAA5A8FD23ACDIE CRC64;
 SQ
 Query Match 81.9%; Score 738; DB 1; Length 174;
 Best Local Similarity 82.2%; Pred. No. 1.7e-59;
 Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
 QY 2 TPLGPASSIPQSFLLKLEQVRKIQGDGALQDEKLCATYKLCHEPELVILGSHLGPAP 61
 DB 1 TPLGPASSIPQSFLLKLEQVRKIQGDGALQDEKLCATYKLCHEPELVILGSHLGPAP 60
 QY 62 LSSCSQALQAGLSQHSGLFLYQGLQALGEGSPLEIPLDTLQDVADPATIMQ 121
 DB 61 LSSCSQALQAGLSQHSGLFLYQGLQALGEGSPLEIPLDTLQDVADPATIMQ 120
 QY 122 MEELGMADALQPTQAGAMPAPAFASFORAGGVLVASHLQSFLEVSYSVLRHLAQP 175
 DB 121 MEDLGVAHVAVQPTQGTMTPTFSAPFRAGGVLVASGLQFLGALRGALRYLAP 174
 RESULT 7
 CSF3_BOVIN
 ID CSF3_BOVIN STANDARD; PRT; 195 AA.
 AC P35833; O9TV89;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CSF3; Synonyms=GCSF;
 OS Bos taurus (bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Holstein;
 RA Heidari M., Kehrl M.E. Jr.;
 RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
 colony stimulating factor."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94076341; PubMed=7504736;
 RA Lovejoy B., Cascio D., Eisenberg D.;
 RT "Crystal structure of canine and bovine granulocyte-colony stimulating
 factor (G-CSF)."
 RL J. Mol. Biol. 234:640-653 (1993).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF092533; AAD16102.1; -
 CC PDB: 1BSC; X-ray; @22-195;
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003629; GCSF_MGF.
 CC InterPro: IPR003573; IL6_MGF_GCSF.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC ProDom: PD008388; GCSF_MGF; 1.
 CC SMART: SM00126; IL6; 1.
 CC DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
 CC FT SIGNAL 1 21 Potential.
 CC FT CHAIN 22 195 Granulocyte colony-stimulating factor.
 CC FT DISULFID 57 63
 CC FT DISULFID 85 95
 CC FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
 CC FT CONFLICT 93 94 TS -> RG (in Ref. 2).
 CC FT HELIX 32 60
 CC FT HELIX 65 69
 CC FT TURN 70 71
 CC FT HELIX 72 75
 CC FT TURN 76 76
 CC FT HELIX 83 85
 CC FT TURN 87 89
 CC FT HELIX 92 112
 CC FT TURN 113 115
 CC FT TURN 118 120
 CC FT HELIX 121 145
 CC FT HELIX 164 191
 CC FT TURN 192 192
 CC SEQUENCE 195 AA; 21431 MW; 8C06119B4ADFBA73 CRC64;
 SQ
 Query Match 80.7%; Score 727; DB 1; Length 195;
 Best Local Similarity 81.0%; Pred. No. 1.9e-58;
 Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 QY 2 TPLGPASSIPQSFLLKLEQVRKIQGDGALQDEKLCATYKLCHEPELVILGSHLGPAP 61
 DB 22 TPLGPASSIPQSFLLKLEQVRKIQGDGALQDEKLCATYKLCHEPELVILGSHLGPAP 81
 QY 62 LSSCSQALQAGLSQHSGLFLYQGLQALGEGSPLEIPLDTLQDVADPATIMQ 121

DB 82 LSSCSQSLQTLSCNLQHLGFLVYQGLQALAGISBELAFTDQLQDVTDFATNIMQ 141
 QY 122 MEELGNAPALQPTQGMAMPAPASAFORRAGGVVYASHQSLFVSYRLRLHAOP 175
 DB 142 MEDLGAAPAVOPQGMPTFTSAFORRAGGVVYASHQSLFVSYRLRLHAOP 195

RESULT 8
 CSF3_PIG STANDARD; PRT; 195 AA.
 ID AC 002837; 019180;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CSF3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae; Sus.
 NCBI_Taxid=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kuhlburg P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RC [2]
 RS TISSUE=Liver;
 RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony stimulating factor."
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC -----
 DR EMBL: Y10494; CAA71518.1; -;
 DR EMBL: U68482; AAB70701.1; -;
 DR EMBL: U68481; AAB70700.1; -;
 DR HSSP: P09919; 1RHG.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR003629; GCSF_MGF.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR SMART: SM00838; GCSF_MGF; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1..21 Potential.
 FT CHAIN 22..195 Granulocyte colony-stimulating factor.
 FT DISULFID 57..63 By similarity.
 FT DISULFID 85..95 By similarity.
 FT CARBOHYD 154..154 O-linked (GalNAc...) (By similarity).
 FT CONFLICT 123..123 A -> R (in Ref. 1).
 FT CONFLICT 123..123 A -> R (in Ref. 1).
 SQ SEQUENCE 195 AA; 21214 MW; 84787F2DBDAEALC CRG4;

Query Match 77.9%; Score 702; DB 1; Length 195;
 Best Local Similarity 79.2%; Pred. No. 3.ee-56;

Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
 QY 3 PLGPASSLPQSFLLKLEQVRIQGGDALQKATYVLCHEPELVILGHSLGIPWAPL 62
 DB 23 PLSPASSLPQSFLLKLEQVRIQGGDALQKATYVLCHEPELVILGHSLGIPWAPL 82
 QY 63 SSCPSQALQAGLCLQSLHSGFLVYQGLQALAGISBELAFTDQLQDVTDFATNIMQ 122
 DB 83 SSCPSQALQAGLCLQSLHSGFLVYQGLQALAGISBELAFTDQLQDVTDFATNIMQ 142

QY 123 EELGNAPALQPTQGMAMPAPASAFORRAGGVVYASHQSLFVSYRLRLHAOP 175
 DB 143 EDLRNAPALQPTQGMPTFTSAFORRAGGVVYASHQSLFVSYRLRLHAOP 195

RESULT 9
 CSF3_MOUSE STANDARD; PRT; 208 AA.
 ID AC P09920;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=Csf3; Synonyms=Csf3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87017003; PubMed=3469940;
 RA Tsuchiya M., Amano S., Kaziro Y., Nagata S.;
 RT "Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor."
 RT Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637 (1986).
 RL (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87190474; PubMed=3494605;
 RX Tsuchiya M., Kaziro Y., Nagata S.;
 RT "The chromosomal gene structure for murine granulocyte colony-stimulating factor."
 RL Eur. J. Biochem. 165:7-12 (1987).
 RN (3)
 RP PARTIAL SEQUENCE.
 RX PubMed=3501294;
 RA Simpson R.J., Nice E.C., Nicola N.A.;
 RT "Structural studies on the murine granulocyte colony-stimulating factor."
 RT Biol. Chem. Hoppe-Seyler 368:1327-1331 (1987).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC -----
 DR EMBL: M13926; AAA37672.1; -;
 DR EMBL: X05402; CAA28986.1; -;
 DR PIR: A29516; A26496.
 DR HSSP: P09919; 1RHG.
 DR InterPro: IPR009079; 4_helix_cytokine.

DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;
 KM Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 208 Granulocyte colony-stimulating factor.
 FT DISULFID 72 78 By similarity.
 FT DISULFID 100 110 By similarity.
 FT CARBOHYD 169 169 O-linked (GalNAc...) (By similarity).
 SQ SEQUENCE 208 AA; 22421 MW; 0BF3622135C906DB CRC64;

Query Match 71.3%; Score 642; DB 1; Length 208;
 Best Local Similarity 74.6%; Pred. No. 1.2e-50;
 Matches 129; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

QY 1 MTPILPSSLPSPFLKLCLEQVRKIQGDGALQEKICATYKLCHEPELVILGHSIGIPWA 60
 DB 36 VSALPSPPLPRSPFLKSLSEQVRKIQASGVLEQICATYKLCHEPELVILGHSIGIPWA 95
 QY 61 PLSSCPSQLQIAGCISQHSGLFLYQGLQALLEGISPELPTLDLTQLDVADPATTIQQ 120
 DB 96 SLSSGSSQALQOTKICISQHSGLFLYQGLQALLEGISPELPTLDLTQLDVADPATTIQQ 155
 QY 121 QMEELGMAPALOPTQGAMPAPAFAPORRAGVIVASHLOSFLVSVRYLRHLAOP 173
 DB 156 QMENIGVAPVPTQPSAMPAPAFAPORRAGVIVASHLOSFLVSVRYLRHLAOP 208

RESULT 10

P97712 PRELIMINARY; PRT; 214 AA.

AC P97712;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Granulocyte colony stimulating factor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=97074656; PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
 RA Han S.W., Ramesh N., Osborne W.R.;
 RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
 stimulating factor";
 RT Gene 175:101-104(1996).
 RL EMBL; U37101; AAC52915.1; -
 DR PIR; JCS043; JCS043.
 DR HSSP; P09919; IRHG.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match 70.5%; Score 635; DB 2; Length 214;
 Best Local Similarity 72.6%; Pred. No. 5.6e-50;
 Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

QY 1 MTPILPSSLPSPFLKLCLEQVRKIQGDGALQEKICATYKLCHEPELVILGHSIGIPWA 60
 DB 27 VSALPSPPLPRSPFLKSLSEQVRKIQARNTLEBQICATYKLCHEPELVILGHSIGIPWA 86
 QY 61 PLSSCPSQLQIAGCISQHSGLFLYQGLQALLEGISPELPTLDLTQLDVADPATTIQQ 120
 DB 87 SLSSGSSQALQOTKICISQHSGLFLYQGLQALLEGISPELPTLDLTQLDVADPATTIQQ 146
 QY 121 QMEELGMAPALOPTQGAMPAPAFAPORRAGVIVASHLOSFLVSVRYLRHLAOP 175
 DB 147 QMENIGVAPVPTQPSAMPAPAFAPORRAGVIVASHLOSFLVSVRYLRHLAOP 201

RESULT 11

Q8MKEO PRELIMINARY; PRT; 127 AA.

AC Q8MKEO;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Granulocyte colony-stimulating factor.
 GN Name=G-CSF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 SEQUENCE FROM N.A.
 RA Noronha L.B., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF503365; AAM34205.1; -
 DR HSSP; P35833; IRG.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSF_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match 56.7%; Score 511; DB 2; Length 127;
 Best Local Similarity 79.5%; Pred. No. 7e-39;
 Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 49 VLHGSLGIPWAPLSSCPSQLQIAGCISQHSGLFLYQGLQALLEGISPELPTLDLTQL 108
 DB 1 MLGHSIGIPWAPLSSCPSQLQIAGCISQHSGLFLYQGLQALLEGISPELPTLDLTQL 60
 QY 109 LDVADPATTIQQMEELGMAPALOPTQGAMPAPAFAPORRAGVIVASHLOSFLVSVRY 168
 DB 61 LDVADPATTIQQMEELGMAPALOPTQGAMPAPAFAPORRAGVIVASHLOSFLVSVRY 120
 QY 169 LRHLAOP 175
 DB 121 LRHLAOP 127

RESULT 12

MGF_CHICK STANDARD; PRT; 201 AA.

AC P13854;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Myelomonocytic growth factor precursor (MGF).
 OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6923161; PubMed=2785450;
 RA Leutz A., Damm K., Sterneck E., Kowenz E., Nees S., Frank R.,
 RA Gausepohl H., Pen Y.-C.E., Smart J., Hayman M., Graf T.;
 RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
 RT reveals relationship to interleukin 6 and granulocyte colony
 RT stimulating factor.";
 RL EMBL J. 8:175-181(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92195319; PubMed=1549124;
 RA Sterneck E., Battner C., Graf T., Leutz A.;
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases.";
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -1- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC -----
 DR EMBL; M85034; AAA48694.1; -;
 DR EMBL; X14477; CA32639.1; -;
 DR PIR; A42247; A42247.
 DR HSSP; P05919; IRHG.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR PRODOM; PD008388; GCSF_MGF; 1.
 DR PRODOM; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR GlycoProtein; Growth factor; Signal.
 FT CHAIN 1 23
 FT SIGNAL 1 23
 FT CHAIN 24 201
 FT DISULFID 61 67
 FT DISULFID 89 99
 FT CARBOHYD 123 123
 FT CARBOHYD 137 137
 FT SEQUENCE 201 AA; 22373 MW; 240A8DD21B424456 CRC64;
 SQ
 Query Match 33.7%; Score 304; DB 1; Length 201;
 Best Local Similarity 40.6%; Pred. No. 1e-19;
 Matches 67; Conservative 26; Mismatches 68; Indels 2; Gaps 1;
 QY 12 QSFLLKLEBOVKIKQGGALQELCATYKLCHEBELVLGHSIGTMAPLSPSQALQ 71
 DB 36 QLFHLNKLLEFTRKIRKRGVALQRAVCDTFLCTEELQLVQDPHVLQAPLDQCHKRFQ 95
 QY 72 IAGCLSLHSGFLFYQGLQALBISPELGPDTLTLQDVADPATTYWOQMEELGMAPAL 131
 DB 96 AAVCFYQIRAGLAHYHSLGAVLRLPRHTTVLTTLQDANLSSNTQQQMEDGLDTVT 155
 QY 132 QPTQ--GAMPAPASAFORRAGVTVASHLOSFILEVSYRVLRHLQ 174

DB 156 LPBAQSPPTSGPFOQOVGGFFLIANFORLETAYRALRIAR 200
 RESULT 13
 ID Q90Y10 PRELIMINARY; PRT; 241 AA.
 AC Q90Y10;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 05-JUN-2004 (TEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 OS Name=IL-6;
 GN Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum";
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ109540; CAC40812.1; -;
 DR EMBL; AJ250838; CAC15566.2; -;
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR PRODOM; PD008388; GCSF_MGF; 1.
 DR PRODOM; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT SIGNAL 1 47
 FT SIGNAL 48 241
 FT CHAIN 48 241
 FT SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 SQ
 Query Match 12.3%; Score 111; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.055;
 Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;
 QY 4 LGPASPSP-----OSFLKLEBOVKIKQGGALQELCATYKLC 44
 DB 41 LPPAAVPLPAAADSSGCVGLERAGARRALDCEPLAVLRRAVOLQDEKCKTVCE 100
 QY 45 PEEVLVLGHSIGTMAPLSSCPQALQAG-----CLQSHSGFLFYQGLQALBISPE 99
 DB 101 NSMELVRRNNLNP-----KYTEDGGLGAFDEKCLITLSSGLFAFQYTLERITGTFDS 156
 QY 100 LGPTLTLQDVADPATTYWOQMEELGMAPALDQPGAMPAPASAFORRAGVTV----- 153
 DB 157 EKQNVESLCYSTGHLLAATIRQWV-----INPDEVLP--DSAQKSLANTKSDKQW 206
 QY 154 ---VASHL-----QSFLEVSRYVLRHL 172
 DB 207 IEKITHLILRDFTSMKTVRAVRYL 233

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RESULT 14
Q8M75 PRELIMINARY; PRT; 212 AA.
ID Q8M75
AC Q8M75
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sub.
OX NCB1_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF518322; NAM74938.1; -.
DR HSSP; P05231; IALU.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMFG.
DR PRODOM; PD00435; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match 12.3%; Score 110.5; DB 2; Length 212;
Best Local Similarity 23.3%; Pred. No. 0.053; Mismatches 85; Indels 5; Gaps 3;
Matches 37; Conservative 32;

QY 17 KCLEVRIQGGALQERKLCATYKLCHEBELVILGHSIGIP-WAPLSCPSQALQLAGC 75
DB 52 KTEBELIKITLIGKISAMRECKEYKRECKENSKVLAENNINLPKMAEKDGCFOGSGFNOETC 111
QY 76 LSQHSGLFLYQGLLQALBEGISPELGPITLDTQLDVAADPATTIWOQMEELGNAPALQPT- 134
DB 112 LMRITTVGLVERQIYLDYLQNEYESNKNVNAEVAQISTKALIQTLRQKKNPDKATTPNPPTT 171
QY 135 -QGAMPAPAS--AFQRRAGCVLVASHLOSFLVSYRVLK 170
DB 172 NAGLLDKLQSQENWKNKTKIILIRSLDFLOFSIRAIR 210

RESULT 15
Q9XT80 PRELIMINARY; PRT; 208 AA.
ID Q9XT80
AC Q9XT80
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCB1_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
RT "Molecular cloning, phylogenetic analysis and expression of beluga
RT whale (Delphinapterus leucas) interleukin 6."
RL EMBL; AF076643; AAD42929.1; -.
DR HSSP; P05231; IALU.
DR GO; GO:0005125; F:cytokine activity; IEA.

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DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMFG.
DR PRODOM; PD00435; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match 12.0%; Score 108; DB 2; Length 208;
Best Local Similarity 21.3%; Pred. No. 0.088; Mismatches 81; Indels 6; Gaps 2;
Matches 33; Conservative 35;

QY 22 VRKIQDGAALQERKLCATYKLCHEBELVILGHSIGIP-WAPLSCPSQALQLAGC 80
DB 52 IKYILGKISAMRECKEYKRECKENSKVLAENNINLPKMAEKDGCFOGSGFNOETC 111
QY 81 SGLFLYQGLLQALBEGISPELGPITLDTQLDVAADPATTIWOQMEELGNAPALQPTQGA--- 137
DB 112 TGLLEYQIYLDYLQNEYESNKNVNAEVAQISTKALIQTLRQKKNPDKATTPNPPTT 171
QY 138 --MPAFASAFQRRAGCVLVASHLOSFLVSYRVLK 170
DB 172 NNLQSQDNDWKNKTKIILIRSLDFLOFSIRAIR 206

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